



SEQUENCE LISTING

#10

<110> APPLICANTS:

(A) Jobling, Stephen Alan
(B) Safford, Richard

<120> TITLE OF INVENTION: Improvements in or Relating to Starch Content of Plants

<130> Case 1637

<140> US 09/297,703

<141> 1999-07-19

<150> PCT/GB97/03032

<151> 1997-11-04

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Glu Thr Val Ser Ile Arg Lys Ile Gly Ser Lys Pro Arg Ser Ile Pro			
125	130	135	
CCA CCC GGC AGA GGG CAA AGA ATA TAT GAC ATA GAT CCA AGC TTG ACA			482
Pro Pro Gly Arg Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser Leu Thr			
140	145	150	
GGC TTT CGT CAA CAC CTA GAT TAC CGG TAT TCA CAG TAC AAA AGA CTC			530
Gly Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu			
155	160	165	170
CGA GAA GAA ATT GAC AAG TAT GAA GGT AGT CTG GAT GCA TTT TCT CGT			578
Arg Glu Glu Ile Asp Lys Tyr Glu Gly Ser Leu Asp Ala Phe Ser Arg			
175	180	185	
GGC TAT GAA AAG TTT GGT TTC TCA CGC AGT GAA ACA GGA ATA ACT TAT			626
Gly Tyr Glu Lys Phe Gly Phe Ser Arg Ser Glu Thr Gly Ile Thr Tyr			
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AGA GAG TGG GCA CCA GGA GCT ACG TGG GCT GCA TTG ATT GGA GAT TTC			674
Arg Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe			
205	210	215	
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Asn Asn Trp Asn Pro Asn Ala Asp Val Met Thr Gln Asn Glu Cys Gly			
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GTC TGG GAG ATC TTT TTG CCG AAT AAT GCA GAT GGT TCA CCA CCA ATT			770
Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile			
235	240	245	250
CCC CAT GGT TCT CGA GTA AAG ATA CGC ATG GAT ACT CCA TCT GGC AAC			818
Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Asn			
255	260	265	
AAA GAT TCT ATT CCT GCT TGG ATC AAG TTC TCA GTT CAA GCA CCA GGT			866
Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly			
270	275	280	
GAA CTC CCA TAT AAT GGC ATA TAC TAT GAT CCT CCC GAG GAG GAG AAG			914
Glu Leu Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys			
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TAT GTG TTC AAA AAT CCT CAG CCA AAG AGA CCA AAA TCA CTT CGG ATT			962
Tyr Val Phe Lys Asn Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile			
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Tyr Glu Ser His Val Gly Met Ser Ser Thr Glu Pro Val Ile Asn Thr			
315	320	325	330
TAT GCC AAC TTT AGA GAT GAT GTG CTT CCT CGC ATC AAA AAG CTT GGC			1058
Tyr Ala Asn Phe Arg Asp Asp Val Leu Pro Arg Ile Lys Lys Leu Gly			

335	340	345	
TAC AAT GCT GTT CAG CTC ATG GCT ATT CAA GAG CAT TCA TAT TAT GCT Tyr Asn Ala Val Gln Leu Met Ala Ile Gln Glu His Ser Tyr Tyr Ala 350	355	360	1106
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ACG TTG GAT GGG CTG AAT ATG TTT GAT GGT ACG GAT GGT CAC TAC TTT Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Gly His Tyr Phe 415	420	425	1298
CAC TCT GGA CCA CGG GGT CAT CAT TGG ATG TGG GAC TCT CGC CTT TTC His Ser Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu Phe 430	435	440	1346
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GTC ACC ATT GGT GAA GAT GTT AGT GGA ATG CCA ACA GTT TGC ATT CCG Val Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Val Cys Ile Pro 525	530	535	1634
GTT GAA GAT GGT GGT GTT GGC TTT GAT TAT CGT CTC CAC ATG GCT GTT Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Val 540	545	550	1682
GCT GAT AAA TGG GTT GAG ATT ATT CAG AAG AGA GAT GAA GAT TGG AAA Ala Asp Lys Trp Val Glu Ile Ile Gln Lys Arg Asp Glu Asp Trp Lys 555	560	565	1730

ATG GGT GAC ATT GTA CAT ATG CTG ACC AAC AGG CGG TGG TTG GAA AAG Met Gly Asp Ile Val His Met Leu Thr Asn Arg Arg Trp Leu Glu Lys 575 580 585	1778
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AAT TTT ATG GGA AAT GAA TTT GGA CAC CCC GAG TGG ATT GAT TTT CCA Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro 655 660 665	2018
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CAT CTG AGA TAT CAT GGA ATG CAA GAG TTT GAT CAA GCA ATT CAG CAT His Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Ile Gln His 700 705 710	2162
CTT GAA GAA GCC TAT GGT TTC ATG ACT TCT GAG CAC CAA TAC ATA TCA Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser 715 720 725 730	2210
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GTT TTT GTA TTC AAT TTT CAT TGG ACT AGC AGC TAT TCG GAT TAC CGA Val Phe Val Phe Asn Phe His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg 750 755 760	2306
GTT GGC TGC TTA AAG CCA GGA AAG TAC AAG ATA GTC TTG GAT TCA GAT Val Gly Cys Leu Lys Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp 765 770 775	2354
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GTG GAG AAT GAA TTG GAA CCT GTC GCC GGT TAA GATATATCTT AACAACAGGT Val Glu Asn Glu Leu Glu Pro Val Ala Gly * 830 835	2551
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<300> WO 98/20145 published 1998-05-14

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Cys Leu Ser Phe Asn Phe Lys Glu Ala Phe Ser Arg Arg Val Phe Ser
35 40 45

Gly Lys Ser Ser His Glu Ser Asp Ser Ser Asn Val Met Val Thr Ala
50 55 60

Ser Lys Arg Val Leu Pro Asp Gly Arg Ile Glu Cys Tyr Ser Ser Ser
65 70 75 80

Thr Asp Gln Leu Glu Ala Pro Gly Thr Val Ser Glu Glu Ser Gln Val
85 90 95

Leu Thr Asp Val Glu Ser Leu Ile Met Asp Asp Lys Ile Val Glu Asp
100 105 110

Glu Val Asn Lys Glu Ser Val Pro Met Arg Glu Thr Val Ser Ile Arg
115 120 125

Lys Ile Gly Ser Lys Pro Arg Ser Ile Pro Pro Pro Gly Arg Gly Gln
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Arg Ile Tyr Asp Ile Asp Pro Ser Leu Thr Gly Phe Arg Gln His Leu
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Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu Arg Glu Glu Ile Asp Lys
165 170 175

Tyr Glu Gly Ser Leu Asp Ala Phe Ser Arg Gly Tyr Glu Lys Phe Gly
180 185 190

Phe Ser Arg Ser Glu Thr Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly
195 200 205

Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe Asn Asn Trp Asn Pro Asn
210 215 220

Ala Asp Val Met Thr Gln Asn Glu Cys Gly Val Trp Glu Ile Phe Leu

225 230 235 240
Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro His Gly Ser Arg Val
245 250 255
Lys Ile Arg Met Asp Thr Pro Ser Gly Asn Lys Asp Ser Ile Pro Ala
260 265 270
Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu Leu Pro Tyr Asn Gly
275 280 285
Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys Tyr Val Phe Lys Asn Pro
290 295 300
Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Ser His Val Gly
305 310 315 320
Met Ser Ser Thr Glu Pro Val Ile Asn Thr Tyr Ala Asn Phe Arg Asp
325 330 335
Asp Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala Val Gln Leu
340 345 350
Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val
355 360 365
Thr Asn Phe Tyr Ala Ala Ser Ser Arg Phe Gly Thr Pro Asp Asp Leu
370 375 380
Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu Leu Val Leu Met
385 390 395 400
Asp Ile Val His Ser His Ala Ser Thr Asn Thr Leu Asp Gly Leu Asn
405 410 415
Met Phe Asp Gly Thr Asp Gly His Tyr Phe His Ser Gly Pro Arg Gly
420 425 430
His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Ser Trp Glu
435 440 445
Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Asp Glu Tyr
450 455 460
Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr
465 470 475 480
His His Gly Leu Gln Val Asp Phe Thr Gly Asn Tyr Asn Glu Tyr Phe
485 490 495
Gly Tyr Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Leu Asn
500 505 510
Asp Met Ile His Gly Leu Phe Pro Glu Ala Val Thr Ile Gly Glu Asp
515 520 525
Val Ser Gly Met Pro Thr Val Cys Ile Pro Val Glu Asp Gly Gly Val

530 535 540
Gly Phe Asp Tyr Arg Leu His Met Ala Val Ala Asp Lys Trp Val Glu
545 550 555 560
Ile Ile Gln Lys Arg Asp Glu Asp Trp Lys Met Gly Asp Ile Val His
565 570 575
Met Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Ser Tyr Ala Glu
580 585 590
Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu
595 600 605
Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr
610 615 620
Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile
625 630 635 640
Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu
645 650 655
Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu
660 665 670
Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys
675 680 685
Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys His Leu Arg Tyr His Gly
690 695 700
Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly
705 710 715 720
Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp
725 730 735
Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe
740 745 750
His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro
755 760 765
Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly
770 775 780
Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp
785 790 795 800
Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr
805 810 815
Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Leu Glu
820 825 830
Pro Val Ala Gly *

835

<210> SEQ ID NO: #30

<211> LENGTH: 3090 base pairs

<212> DNA

<213> genus, species

<220>

<221> CDS

<222> 131..2677

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #30

AGTGAATTG AGCTCGGTAC CCGGGGATCC GATTCGCATT TCTCGCTATT GCTTTCCGTT 60

TATTTCCATA TATAAAATAT CAAATCTAAT CACTTGCGCC ATTTCTATCT CTCTCCAAAC 120

TCTCACCGAA ATG GTA TAC ACT GTA TCA GGC ATA CGT TTT CCT TGT 169
Met Val Tyr Tyr Thr Val Ser Gly Ile Arg Phe Pro Cys
840 845 850

GCA CCT TCA CTC TAC AAA TCT CAG CTC ACC AGC TTC CAT GGC GGT CGA 217
Ala Pro Ser Leu Tyr Lys Ser Gln Leu Thr Ser Phe His Gly Arg

855	860	865	
AGG ACC TCT TCT GGC CTT TCC TTC CTC TTG AAG AAG GAG CTG TTT CCT Arg Thr Ser Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro 870	875	880	265
CGG AAG ATC TTT GCT GGA AAG TCC TCT TAT GAA TCT GAC TCC TCA AAT Arg Lys Ile Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn 885	890	895	313
TTA ACT GTC TCT GCA TCT GAG AAG GTC CTT GTT CCT GAT GAT CAG ATT Leu Thr Val Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile 900	905	910	361
GAT GGC TCT TCT TCA ACA TAT CAA TTA GAA ACC ACT GGC ACA GTT Asp Gly Ser Ser Ser Thr Tyr Gln Leu Glu Thr Thr Gly Thr Val 915	920	925	409
TTG GAG GAA TCC CAG GTT CTT GGT GAT GCA GAG AGT CTT GTG ATG GAA Leu Glu Glu Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu 935	940	945	457
GAT GAT AAG AAT GTT GAG GAG GAT GAA GTA AAA AAA GAG TCG GTT CCA Asp Asp Lys Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro 950	955	960	505
TTG CAT GAG ACA ATT AGC ATT GGA AAA AGT GAA TCT AAA CCA AGG TCC Leu His Glu Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser 965	970	975	553
ATT CCT CCA CCT GGC AGT GGG CAG AGA ATA TAT GAC ATA GAT CCA AGC Ile Pro Pro Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser 980	985	990	601
TTG GCA GGT TTC CGT CAG CAT CTT GAC TAC CGA TAT TCA CAG TAC AAA Leu Ala Gly Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys 995	1000	1005	649
AGG CTG CGT GAG GAA ATT GAC AAG TAT GAA GGT GGT TTG GAT GCA TTC Arg Leu Arg Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe 1015	1020	1025	697
TCT CGT GGA TTT GAA AAG TTT GGT TTC TTA CGC AGT GAA ACA GGA ATA Ser Arg Gly Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile 1030	1035	1040	745
ACT TAT AGG GAA TGG GCA CCT GGA GCT ACG TGG GCT GCA CTT ATT GGA Thr Tyr Arg Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly 1045	1050	1055	793
GAT TTC AAC AAT TGG AAT CCT AAT GCA GAT GTC ATG ACT CGG AAT GAG Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu 1060	1065	1070	841
TTT GGT GTC TGG GAG ATT TTT TTG CCA AAT AAC GCA GAT GGT TCA CCA Phe Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro 1075	1080	1085	889
		1090	

CCA ATT CCT CAT GGT TCT CGA GTA AAG ATA CGC ATG GAT ACT CCA TCT Pro Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser 1095 1100 1105	937
GGC ATC AAA GAT TCA ATT CCT GCT TGG ATC AAG TTC TCA GTT CAG GCA Gly Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala 1110 1115 1120	985
CCT GGT GAA ATC CCA TAC AAT GCC ATA TAC TAT GAT CCA CCA AAG GAG Pro Gly Glu Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu 1125 1130 1135	1033
GAG AAG TAT GTG TTC AAA CAT CCT CAG CCA AAG AGA CCA AAA TCA CTT Glu Lys Tyr Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu 1140 1145 1150	1081
AGG ATT TAT GAA TCT CAT GTT GGG ATG AGT AGT ATG GAG CCA ATA ATT Arg Ile Tyr Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile 1155 1160 1165 1170	1129
AAC ACA TAT GCC AAC TTT AGA GAT GAT ATG CTT CCT CGC ATC AAA AAG Asn Thr Tyr Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys 1175 1180 1185	1177
CTT GGC TAC AAT GCT GTT CAG ATC ATG GCT ATT CAA GAG CAT TCC TAT Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr 1190 1195 1200	1225
TAT GCT AGT TTT GGG TAC CAT GTC ACA AAC TTT TTT GCA CCT AGC AGC Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser 1205 1210 1215	1273
CGA TTT GGA ACT CCT GAT GAT TTG AAG TCT TTA ATA GAT AAA GCT CAT Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His 1220 1225 1230	1321
GAG TTA GGG CTG CTT GTT CTC ATG GAT ATT GTT CAT AGC CAT GCG TCA Glu Leu Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser 1235 1240 1245 1250	1369
AAT AAT ACG TTG GAT GGG CTG AAC ATG TTT GAT GGT ACG GAT AGT CAC Asn Asn Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His 1255 1260 1265	1417
TAC TTC CAC TCC GGA TCA CGG GGT CAT CAT TGG TTG TGG GAC TCT CGC Tyr Phe His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg 1270 1275 1280	1465
CTT TTC AAC TAT GGA AGC TGG GAG GTG CTA AGA TTT CTT CTT TCA AAT Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn 1285 1290 1295	1513
GCA AGA TGG TGG TTG GAA GAG TAC AGG TTT GAT GGT TTT AGA TTT GAT Ala Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp 1300 1305 1310	1561

GGG GTG ACT TCC ATG ATG TAC ACT CCC CAT GGG TTG CAG GTA GCT TTT Gly Val Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe 1315 1320 1325 1330	1609
ACT GGC AAC TAC AAT GAG TAC TTT GGA TAT GCA ACT GAT GTA GAT GCT Thr Gly Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala 1335 1340 1345	1657
GTG ATT TAT TTG ATG CTT GTG AAT GAT ATG ATT CAC GGT CTT TTC CCT Val Ile Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro 1350 1355 1360	1705
GAG GCT GTT ACC ATT GGT GAA GAT GTT AGC GGA AAG CCA ACA TTT TGC Glu Ala Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys 1365 1370 1375	1753
ATT CCA GTG GAA GAT GGT GTT GGA TTT GAT TAC CGT CTC CAC ATG Ile Pro Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met 1380 1385 1390	1801
GCC ATT GCC GAT AAA TGG ATT GAG ATT CTT AAG AAG AGA GAT GAG GAC Ala Ile Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp 1395 1400 1405 1410	1849
TGG AAA ATG GGT GAC ATT GTG CAT ACA CTC ACC AAC AGA AGG TGG TTG Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu 1415 1420 1425	1897
GAA AAA TGT GTT GCT TAT GCT GAA AGT CAT GAC CAA GCT CTT GTT GGT Glu Lys Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly 1430 1435 1440	1945
GAC AAA ACT ATT GCA TTT TGG CTG ATG GAC AAG GAC ATG TAC GAC TTC Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe 1445 1450 1455	1993
ATG GCT CGT GAC AGA CCA TCT ACT CCT CTT ATA GAT CGT GGA ATA GCA Met Ala Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala 1460 1465 1470	2041
TTG CAC AAA ATG ATC AGG CTT ATT ACC ATG GGC TTA GGC GGA GAA GGA Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly 1475 1480 1485 1490	2089
TAT TTG AAT TTT ATG GGA AAT GAA TTT GGA CAT CCT GAG TGG ATT GAT Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp 1495 1500 1505	2137
TTT CCA AGA GGG GAT CGA CAT CTG CCC AAT GGT AAA GTA ATT CCA GGG Phe Pro Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly 1510 1515 1520	2185
AAC AAC CAC AGT TAT GAT AAA TGC CGT CGT AGA TTT GAT CTA GGT GAT Asn Asn His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp 1525 1530 1535	2233
GCA GAC TAT CTA AGA TAT CAT GGA ATG CAA GAG TTT GAT CAG GCA ATG	2281

Ala Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met			
1540	1545	1550	
CAA CAT CTT GAA GAA GCC TAT GGT TTC ATG ACT TCT GAG CAC CAG TAT			2329
Gln His Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr			
1555	1560	1565	1570
ATA TCA CGG AAG GAT GAA GGA GAT CGG ATC ATT GTC TTT GAG AGG GGA			2377
Ile Ser Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly			
1575	1580	1585	
AAC CTT GTT TTT GTA TTC AAC TTT CAT TGG ACT AAC AGC TAT TCA GAT			2425
Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp			
1590	1595	1600	
TAC CGA GTT GGC TGC TTC AAG TCA GGA AAG TAC AAG ATT GTT TTG GAC			2473
Tyr Arg Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp			
1605	1610	1615	
TCG GAT GAT GGC TTG TTT GGA GGC TTC AAC AGG CTT AGT CAT GAT GCC			2521
Ser Asp Asp Gly Leu Phe Gly Phe Asn Arg Leu Ser His Asp Ala			
1620	1625	1630	
GAG CAC TTC ACC TTT GAC GGG TGG TAT GAT AAC CGG CCT CGG TCC TTC			2569
Glu His Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe			
1635	1640	1645	1650
ATG GTA TAT GCA CCA TCT AGG ACA GCA GTG GTC TAT GCT TTA GTA GAA			2617
Met Val Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu			
1655	1660	1665	
GAT GAA GAG AAT GAA GCA GAG AAT GAA GTA GAA AGT GAA GTG AAA CCA			2665
Asp Glu Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro			
1670	1675	1680	
GCC TCC GGC TGA GATAGATATT TAGTAAGAGG ATCCCCTAAA GCAGGAATGG			2717
Ala Ser Gly *			
1685			
TTAACCTGTG CATCTGCATT GAACGACGTA TATTGAGACT TGAATTGATT TGCTGCTCAG			2777
GACACAGAAT ATTAATTCCA AGGCTCAAGG CAGAGATACA CGCCATAATG CATGATCATA			2837
TGAAAGCTCC CCAAATTGTA AATCATTAG CAAGCTGCGT GCACTCTGTA AATTATATGT			2897
AGTACTTTGG CAAGTCACGT TATTATGGAT ACCATGGATG TCCGCTAGGA AAAATTTGT			2957
GTATACGCCT ACTAGGATTT TTAAATCTCG CATGTTCCAC ATAAAGTGGT GGTTGAATGT			3017
TGCGCGACTA TTTTGAGTA AAATGATTGA AGTTATTCTT CACTTGGGCC TGTGAAAAAA			3077
AAAAAAAAAA AAA			3090

<210> SEQ ID NO: #31

<211> LENGTH: 849 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #31

Met Val Tyr Tyr Thr Val Ser Gly Ile Arg Phe Pro Cys Ala Pro Ser
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Leu Tyr Lys Ser Gln Leu Thr Ser Phe His Gly Gly Arg Arg Thr Ser
20 25 30

Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro Arg Lys Ile
35 40 45

Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn Leu Thr Val
50 55 60

Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile Asp Gly Ser
65 70 75 80

Ser Ser Ser Thr Tyr Gln Leu Glu Thr Gly Thr Val Leu Glu Glu

85

90

95

Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu Asp Asp Lys
100 105 110

Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro Leu His Glu
115 120 125

Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser Ile Pro Pro
130 135 140

Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser Leu Ala Gly
145 150 155 160

Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu Arg
165 170 175

Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe Ser Arg Gly
180 185 190

Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile Thr Tyr Arg
195 200 205

Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe Asn
210 215 220

Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu Phe Gly Val
225 230 235 240

Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro
245 250 255

His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Ile Lys
260 265 270

Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu
275 280 285

Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu Glu Lys Tyr
290 295 300

Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr
305 310 315 320

Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile Asn Thr Tyr
325 330 335

Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys Leu Gly Tyr
340 345 350

Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser
355 360 365

Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly
370 375 380

Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly

385 390 395 400
Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn Thr
405 410 415
Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe His
420 425 430
Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe Asn
435 440 445
Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp
450 455 460
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
465 470 475 480
Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly Asn
485 490 495
Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile Tyr
500 505 510
Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala Val
515 520 525
Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro Val
530 535 540
Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile Ala
545 550 555 560
Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys Met
565 570 575
Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys
580 585 590
Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr
595 600 605
Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Arg
610 615 620
Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys
625 630 635 640
Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn
645 650 655
Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg
660 665 670
Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn His
675 680 685
Ser Tyr Asp Lys Cys Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr

690 695 700
Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu
705 710 715 720
Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg
725 730 735
Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val
740 745 750
Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Val
755 760 765
Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp
770 775 780
Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His Phe
785 790 795 800
Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr
805 810 815
Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu Asp Glu Glu
820 825 830
Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser Gly
835 840 845

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<210> SEQ ID NO: #32

<211> LENGTH: 48 base pairs

<212> DNA

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #32
GGAAATCCAT ATGACTAGTA GATCCTCTAG AGTCGACCTG CAGGCATG 48

<210> SEQ ID NO: #33

<211> LENGTH: 1069 base pairs

<212> DNA

<213> genus, species

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<221> CDS

<222> 1..687

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<300> WO 98/20145 published 1998-05-14

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ATG GAC AAG GAT ATG TAT GAC TTC ATG GCT CTT GAC AGA CCA TCT ACT	48
Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr	
1 5 10 15	
CCT CTC ATA GAT CGT GGA GTA GCA TTG CAC AAA ATG ATC AGG CTT ATT	96
Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile	
20 25 30	
ACC ATG GGA TTA GGC GGA GAA GGA TAT TTG AAT TTT ATG GGA AAT GAA	144
Thr Met Gly Leu Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu	
35 40 45	
TTT GGA CAC CCC GAG TGG ATT GAT TTT CCA AGA GGT GAT CTA CAT CTT	192
Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu	
50 55 60	
CCC AGT GGT AAA TTT GTT CCT GGG AAC AAT TAC AGT TAT GAT AAA TGC	240
Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys	
65 70 75 80	
CGG CGT AGG TTT GAT CTA GGC AAT TCA AAG CGT CTG AGA TAT CAT GGA	288
Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly	
85 90 95	
ATG CAA GAG TTT GAT CAA GCA ATT CAG CAT CTT GAA GAA GCC TAT GGT	336
Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly	
100 105 110	
TTC ATG ACT TCT GAG CAC CAA TAC ATA TCA CGG AAG GAT GAA AGG GAT	384
Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp	
115 120 125	
CGG ATC ATT GTC TTC GAG AGG GGA AAC CTC GTT TTT GTA TTC AAT TTT	432
Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe	
130 135 140	
CAT TGG ACT AGC AGC TAT TCG GAT TAC CGA GTT GGC TGC TTA AAG CCA	480
His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro	
145 150 155 160	
GGA AAG TAC AAG ATA GTC TTG GAT TCA GAT GAT CCT TTG TTT GGA GGC	528
Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly	
165 170 175	
TTT GGC AGG CTT AGT CAT GAT GCA GAG CAC TTC AGC TTT GAA GGG TGG	576
Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp	
180 185 190	
TAC GAT AAC CGG CCT CGA TCC TTC ATG GTG TAC ACA CCA TGT AGA ACA	624

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr
195 200 205

GCA GTG GTC TAT GCT TTA GTG GAG GAT GAA GTG GAG AAT GAA GTG GAA 672
Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu
210 215 220

CCT GTC GCC GGT TAA GATATATCTT AGCAACAGGT TCTGAAGCAG GAATGCCATT 727
Pro Val Ala Gly *
225

ATTGATCTTC CTATGTGCAT CTGCGTTGAA CGAAATATAT TGAGCCTATA ATTTGATGTC 787
ACGGTCCTTG CAGATTCCA TCCTGGTTCT TGGTATTTG TTGTCATGAT AAACATAATC 847
AAAGACCAAT AGGAAACGCA GGGTTACATG CTAGCTTCCA TCATCATAGG GAGCTCAGAC 907
CTCCTAAACC ATAAATCTTC AAGCTGCCTG CGTTCGGTAG TATGTTATGT GGTACTTTGC 967
AATCTTAAAT TATCATGATC GCTGTGGATG CTAACTATGA CAATTTGTA TATATGCCAA
CGAGGATTAA AAGTTTAAA AAAAAAACAA AAAAAATCCA TG 1027
1069

<210> SEQ ID NO: #34

<211> LENGTH: 229 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #34

Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr
1 5 10 15

Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile
20 25 30

Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu
35 40 45

Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu
50 55 60

Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys
65 70 75 80

Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly
85 90 95

Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly
100 105 110

Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp
115 120 125

Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe
130 135 140

His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro
145 150 155 160

Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly
165 170 175

Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp
180 185 190

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr
195 200 205

Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu
210 215 220

Pro Val Ala Gly *
225

<210> SEQ ID NO: #35

<211> LENGTH: 1919 base pairs
<212> DNA
<213> genus, species
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<221> CDS
<222> 61..1506
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<300> WO 98/20145 published 1998-05-14
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TATGGATTGA CATCGATAAT ACGACTCACT ATAGGGATTT TTTTTTTTTT TTTTTTTGT 60
AGT TTT GGG TAC CAT GTC ACA AAC TTT TTT GCA CCT AGC AGC CGA TTT 108
Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe
230 235 240 245
GGA ACT CCT GAT GAT TTG AAG TCT TTA ATA GAT AAA GCT CAT GAG TTA 156
Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu
250 255 260
GGG CTG CTT GTT CTC ATG GAT ATT GTT CAT AGC CAT GCG TCA AAT AAT 204
Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn
265 270 275

ACG TTG GAT GGG CTG AAC ATG TTT GAT GGT ACG GAT AGT CAC TAC TTC			252
Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe	280	285	
280	285	290	
CAC TCC GGA TCA CGG GGT CAT CAT TGG TTG TGG GAC TCT CGC CTT TTC			300
His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe	295	300	
295	300	305	
AAC TAT GGA AGC TGG GAG GTG CTA AGA TTT CTT CTT TCA AAT GCA AGA			348
Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg	310	315	
310	315	320	
325			
TGG TGG TTG GAA GAG TAC AGG TTT GAT GGT TTT AGA TTT GAT GGG GTG			396
Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val	330	335	
330	335	340	
ACT TCC ATG ATG TAC ACT CCC CAT GGG TTG CAG GTA GCT TTT ACT GGC			444
Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly	345	350	
345	350	355	
AAC TAC AAT GAG TAC TTT GGA TAT GCA ACT GAT GTA GAT GCT GTG ATT			492
Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile	360	365	
360	365	370	
TAT TTG ATG CTT GTG AAT GAT ATG ATT CAC GGT CTT TTC CCT GAG GCT			540
Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala	375	380	
375	380	385	
GTT ACC ATT GGT GAA GAT GTT AGC GGA AAG CCA ACA TTT TGC ATT CCA			588
Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro	390	395	
390	395	400	
405			
GTG GAA GAT GGT GGT GTT GGA TTT GAT TAC CGT CTC CAC ATG GCC ATT			636
Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile	410	415	
410	415	420	
GCC GAT AAA TGG ATT GAG ATT CTT AAG AAG AGA GAT GAG GAC TGG AAA			684
Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys	425	430	
425	430	435	
ATG GGT GAC ATT GTG CAT ACA CTC ACC AAC AGA AGG TGG TTG GAA AAA			732
Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys	440	445	
440	445	450	
TGT GTT GCT TAT GCT GAA AGT CAT GAC CAA GCT CTT GTT GGT GAC AAA			780
Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys	455	460	
455	460	465	
ACT ATT GCA TTT TGG CTG ATG GAC AAG GAC ATG TAC GAC TTC ATG GCT			828
Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala	470	475	
470	475	480	
485			
CGT GAC AGA CCA TCT ACT CCT CTT ATA GAT CGT GGA ATA GCA TTG CAC			876
Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His	490	495	
490	495	500	

AAA ATG ATC AGG CTT ATT ACC ATG GGC TTA GGC GGA GAA GGA TAT TTG Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu 505 510 515	924
AAT TTT ATG GGA AAT GAA TTT GGA CAT CCT GAG TGG ATT GAT TTT CCA Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro 520 525 530	972
AGA GGG GAT CGA CAT CTG CCC AAT GGT AAA GTA ATT CCA GGG AAC AAC Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn 535 540 545	1020
CAC AGT TAT GAT AAA TGC CGT CGT AGA TTT GAT CTA GGT GAT GCA GAC His Ser Tyr Asp Lys Cys Arg Arg Phe Asp Leu Gly Asp Ala Asp 550 555 560 565	1068
TAT CTA AGA TAT CAT GGA ATG CAA GAG TTT GAT CAG GCA ATG CAA CAT Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His 570 575 580	1116
CTT GAA GAA GCC TAT GGT TTC ATG ACT TCT GAG CAC CAG TAT ATA TCA Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser 585 590 595	1164
CGG AAG GAT GAA GGA GAT CGG ATC ATT GTC TTT GAG AGG GGA AAC CTT Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu 600 605 610	1212
GTT TTT GTA TTC AAC TTT CAT TGG ACT AAC AGC TAT TCA GAT TAC CGA Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg 615 620 625	1260
GTT GGC TGC TTC AAG TCA GGA AAG TAC AAG ATT GTT TTG GAC TCG GAT Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp 630 635 640 645	1308
GAT GGC TTG TTT GGA GGC TTC AAC AGG CTT AGT CAT GAT GCC GAG CAC Asp Gly Leu Phe Gly Phe Asn Arg Leu Ser His Asp Ala Glu His 650 655 660	1356
TTC ACC TTT GAC GGG TGG TAT GAT AAC CGG CCT CGG TCC TTC ATG GTA Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val 665 670 675	1404
TAT GCA CCA TCT AGG ACA GCA GTG GTC CAT GCT TTA GTA GAA GAT GAA Tyr Ala Pro Ser Arg Thr Ala Val Val His Ala Leu Val Glu Asp Glu 680 685 690	1452
GAG AAT GAA GCA GAG AAT GAA GTA GAA AGT GAA GTG AAA CCA GCC TCC Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser 695 700 705	1500
GGC TGA GATAGATATT TAGTAAGAGG ATCCCCTAAA GCAGGAATGG TTAACCTGTG Gly * 710	1556
CATCTGCATT GAACGACGTA TATTGAGACT TGAATTGATT TGCTGCTCAG GACACAGAAT	1616

ATTAATTCCA AGGCTCAAGG CAGAGATACA CGCCATAATG CATGATCATA TGAAAGCTCC	1676
CCAACTTGTA AATCATTAG CAAGCTGCGT GCACTCTGTA AATTATATGT AGTACTTTGG	1736
CAAGTCACGT TATTATGGAT ACCATGGATG TCCGCTAGGA AAAATTTGT GTATACGCCT	1796
ACTAGGATT TTAAATCTCG CATGTTCCAC ATAAAGTGGT GGTTGAATGT TGCGCGACTA	1856
TTTTGAGTA AAATGATTGA AGTTATTCTT CACTGGGCC TGTGAAAAAA AAAAAAAAAA	1916
AAA	1919

<210> SEQ ID NO: #36

<211> LENGTH: 482 amino acids

<212> PRT

<213> genus, species

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<300> WO 98/20145 published 1998-05-14

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<400> SEQ ID NO: #36

Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe
1 5 10 15

Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu
20 25 30

Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn
35 40 45

Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe
50 55 60

His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe
65 70 75 80

Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg
85 90 95

Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val
100 105 110

Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly
115 120 125

Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile
130 135 140

Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala
145 150 155 160

Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro
165 170 175

Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile
180 185 190

Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys
195 200 205

Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys
210 215 220

Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys
225 230 235 240

Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala
245 250 255

Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His
260 265 270

Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu
275 280 285

Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro
290 295 300

Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn
305 310 315 320

His Ser Tyr Asp Lys Cys Arg Arg Phe Asp Leu Gly Asp Ala Asp
325 330 335

Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His
340 345 350

Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser
355 360 365

Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu
370 375 380

Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg
385 390 395 400

Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp
405 410 415

Asp Gly Leu Phe Gly Phe Asn Arg Leu Ser His Asp Ala Glu His
420 425 430

Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val
435 440 445

Tyr Ala Pro Ser Arg Thr Ala Val Val His Ala Leu Val Glu Asp Glu
450 455 460

Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser
465 470 475 480

Gly *